SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (I) APPLICANT: Rothe, Mike
                 Goeddel, David V

  (ii) TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

 (iii) NUMBER OF SEQUENCES: 14

  (iv) CORRESPONDENCE ADDRESS:
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    (C) CITY: San Francisco
    (D) STATE: California
    (E) COUNTRY: USA
    (F) ZIP: 94111

   (v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Floppy disk
    (B) COMPUTER: IBM PC compatible
    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER: US
    (B) FILING DATE:
    (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME:Brezner, David J.
    (B) REGISTRATION NUMBER: 24,774
    (C) REFERENCE/DOCKET NUMBER: A-62464/DJB

  (ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: (415)781-1989
    (B) TELEFAX: (415)398-3249

(2) INFORMATION FOR SEQ ID NO:1:

    (I) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 2589 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAAGTAGT ATCTTGGAAA TTCAGAGAGA TACTCATCCT ACCTGAATAT AAACTGAGAT   60

AAATCCAGTA AAGAAAGTGT AGTAAATTCT ACATAAGAGT CTATCATTGA TTTCTTTTGG   120

```
TGGTAAAAAT CTTAGTTCAT GTGAAGAAAT TTCATGTGAA TGTTTTAGCT ATCAAACAGC          180

ACTGTCACCT ACTCATGCAC AAAACTGCCT CCCAAAGACT TTTCCCAGGT CCCTCGTATC          240

AAAACATTAA GAGTATAATG GAAGATAGCA CGATCTTGTC AGATTGGACA AACAGCAACA          300

AACAAAAAAT GAAGTATGAC TTTTCCTGTG AACTCTACAG AATGTCTACA TATTCAACTT          360

TCCCCGCCGG GGTGCCTGTC TCAGAAAGGA GTCTTGCTCG TGCTGGTTTT TATTATACTG          420

GTGTGAATGA CAAGGTCAAA TGCTTCTGTT GTGGCCTGAT GCTGGATAAC TGGAAACTAG          480

GAGACAGTCC TATTCAAAAG CATAAACAGC TATATCCTAG CTGTAGCTTT ATTCAGAATC          540

TGGTTTCAGC TAGTCTGGGA TCCACCTCTA AGAATACGTC TCCAATGAGA AACAGTTTTG          600

CACATTCATT ATCTCCCACC TTGGAACATA GTAGCTTGTT CAGTGGTTCT TACTCCAGCC          660

TTTCTCCAAA CCCTCTTAAT TCTAGAGCAG TTGAAGACAT CTCTTCATCG AGGACTAACC          720

CCTACAGTTA TGCAATGAGT ACTGAAGAAG CCAGATTTCT TACCTACCAT ATGTGGCCAT          780

TAACTTTTTT GTCACCATCA GAATTGGCAA GAGCTGGTTT TTATTATATA GGACCTGGAG          840

ATAGGGTAGC CTGCTTTGCC TGTGGTGGGA AGCTCAGTAA CTGGGAACCA AAGGATGATG          900

CTATGTCAGA ACACCGGAGG CATTTTCCCA ACTGTCCATT TTTGGAAAAT TCTCTAGAAA          960

CTCTGAGGTT TAGCATTTCA AATCTGAGCA TGCAGACACA TGCAGCTCGA ATGAGAACAT         1020

TTATGTACTG GCCATCTAGT GTTCCAGTTC AGCCTGAGCA GCTTGCAAGT GCTGGTTTTT         1080

ATTATGTGGG TCGCAATGAT GATGTCAAAT GCTTTTGTTG TGATGGTGGC TTGAGGTGTT         1140

GGGAATCTGG AGATGATCCA TGGGTAGAAC ATGCCAAGTG GTTTCCAAGG TGTGAGTTCT         1200

TGATACGAAT GAAAGGCCAA GAGTTTGTTG ATGAGATTCA AGGTAGATAT CCTCATCTTC         1260

TTGAACAGCT GTTGTCAACT TCAGATACCA CTGGAGAAGA AAATGCTGAC CCACCAATTA         1320

TTCATTTTGG ACCTGGAGAA AGTTCTTCAG AAGATGCTGT CATGATGAAT ACACCTGTGG         1380

TTAAATCTGC CTTGGAAATG GGCTTTAATA GAGACCTGGT GAAACAAACA GTTCAAAGTA         1440

AAATCCTGAC AACTGGAGAG AACTATAAAA CAGTTAATGA TATTGTGTCA GCACTTCTAA         1500

ATGCTGAAGA TGAAAAAAGA GAGGAGGAGA AGGAAAAACA AGCTGAAGAA ATGGCATCAG         1560

ATGATTTGTC ATTAATTCGG AAGAACAGAA TGGCTCTCTT TCAACAATTG ACATGTGTGC         1620

TTCCTATCCT GGATAATCTT TTAAAGGCCA ATGTAATTAA TAAACAGGAA CATGATATTA         1680

TTAAACAAAA AACACAGATA CCTTTACAAG CGAGAGAACT GATTGATACC ATTTTGGTTA         1740

AAGGAAATGC TGCGGCCAAC ATCTTCAAAA ACTGTCTAAA AGAAATTGAC TCTACATTGT         1800

ATAAGAACTT ATTTGTGGAT AAGAATATGA AGTATATTCC AACAGAAGAT GTTTCAGGTC         1860
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TGTCACTGGA AGAACAATTG AGGAGGTTGC AAGAAGAACG AACTTGTAAA GTGTGTATGG      1920

ACAAAGAAGT TTCTGTTGTA TTTATTCCTT GTGGTCATCT GGTAGTATGC CAGGAATGTG      1980

CCCCTTCTCT AAGAAAATGC CCTATTTGCA GGGGTATAAT CAAGGGTACT GTTCGTACAT      2040

TTCTCTCTTA AAGAAAAATA GTCTATATTT TAACCTGCAT AAAAAGGTCT TTAAAATATT      2100

GTTGAACACT TGAAGCCATC TAAAGTAAAA AGGGAATTAT GAGTTTTTCA ATTAGTAACA      2160

TTCATGTTCT AGTCTGCTTT GGTACTAATA ATCTTGTTTC TGAAAAGATG GTATCATATA      2220

TTTAATCTTA ATCTGTTTAT TTACAAGGGA AGATTTATGT TTGGTGAACT ATATTAGTAT      2280

GTATGTGTAC CTAAGGGAGT AGTGTCACTG CTTGTTATGC ATCATTTCAG GAGTTACTGG      2340

ATTTGTTGTT CTTTCAGAAA GCTTTGAATA CTAAATTATA GTGTAGAAAA GAACTGGAAA      2400

CCAGGAACTC TGGAGTTCAT CAGAGTTATG GTGCCGAATT GTCTTTGGTG CTTTTCACTT      2460

GTGTTTTAAA ATAAGGATTT TTCTCTTATT TCTCCCCCTA GTTTGTGAGA AACATCTCAA      2520

TAAAGTGCTT TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      2580

AAAAAAAAA                                                            2589
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 618 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
1               5                   10                  15

Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
            20                  25                  30

Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
            35                  40                  45

Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
    50                  55                  60

Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
65                  70                  75                  80

Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
                85                  90                  95
```

```
Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe
             100             105             110

Ile Gln Asn Leu Val Ser Ala Ser Leu Gly Ser Thr Ser Lys Asn Thr
         115             120             125

Ser Pro Met Arg Asn Ser Phe Ala His Ser Leu Ser Pro Thr Leu Glu
         130             135             140

His Ser Ser Leu Phe Ser Gly Ser Tyr Ser Ser Leu Ser Pro Asn Pro
145             150             155             160

Leu Asn Ser Arg Ala Val Glu Asp Ile Ser Ser Ser Arg Thr Asn Pro
             165             170             175

Tyr Ser Tyr Ala Met Ser Thr Glu Glu Ala Arg Phe Leu Thr Tyr His
             180             185             190

Met Trp Pro Leu Thr Phe Leu Ser Pro Ser Glu Leu Ala Arg Ala Gly
         195             200             205

Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys Gly
    210             215             220

Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asp Ala Met Ser Glu His
225             230             235             240

Arg Arg His Phe Pro Asn Cys Pro Phe Leu Glu Asn Ser Leu Glu Thr
             245             250             255

Leu Arg Phe Ser Ile Ser Asn Leu Ser Met Gln Thr His Ala Ala Arg
             260             265             270

Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro Val Gln Pro Glu
         275             280             285

Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp Asp Val
    290             295             300

Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser Gly Asp
305             310             315             320

Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg Cys Glu Phe Leu
             325             330             335

Ile Arg Met Lys Gly Gln Glu Phe Val Asp Glu Ile Gln Gly Arg Tyr
         340             345             350

Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Thr Thr Gly Glu
    355             360             365

Glu Asn Ala Asp Pro Pro Ile Ile His Phe Gly Pro Gly Glu Ser Ser
    370             375             380

Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
385             390             395             400
```

```
Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Gln Ser Lys
            405             410             415

Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
            420             425             430

Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Glu Lys Glu Lys
            435             440             445

Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
    450             455             460

Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
465             470             475             480

Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile
            485             490             495

Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
            500             505             510

Ile Leu Val Lys Gly Asn Ala Ala Ala Asn Ile Phe Lys Asn Cys Leu
            515             520             525

Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
    530             535             540

Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
545             550             555             560

Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
            565             570             575

Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val Cys
            580             585             590

Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile
    595             600             605

Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
610             615
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2601 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCAGCAGG TTTACAAAGG AGGAAAACGA CTTCTTCTAG ATTTTTTTTT CAGTTCTTC   60

```
TATAAATCAA AACTACCTCC CTAGAGAAAG GCTAGTCCCT TTTCTTCCCC ATTCATTTCA      120

TTATGAACAT AGTAGAAAC AGCATATTCT TATCAAATTT GATGAAAGC GCCAACACGT        180

TTGAACTGAA ATACGACTTG TCATGTGAAC TGTACCGAAT GTCTACGTAT TCCACTTTTC      240

CTGCTGGGGT CCCTGTCTCA GAAAGGAGTC TTGCTCGCGC TGGTTTCTAT TACACTGGTG      300

TGAATGACAA GGTCAAATGC TTCTGTTGTG GCCTGATGCT GGATAACTGG AAAAGAGGAG      360

ACAGTCCTAC TGAAAAGCAT AAAAAGTTGT ATCCTAGCTG CAGATTCGTT CAGAGTCTAA      420

ATTCCGTTAA CAACTTGGAA GCTACCTCTC AGCCTACTTT TCCTTCTTCA GTAACAAATT      480

CCACACACTC ATTACTTCCG GGTACAGAAA ACAGTGGATA TTTCCGTGGC TCTTATTCAA      540

ACTCTCCATC AAATCCTGTA AACTCCAGAG CAAATCAAGA TTTTTCTGCC TTGATGAGAA      600

GTTCCTACCA CTGTGCAATG AATAACGAAA ATGCCAGATT ACTTACTTTT CAGACATGGC      660

CATTGACTTT TCTGTCGCCA ACAGATCTGG CAAAAGCAGG CTTTTACTAC ATAGGACCTG      720

GAGACAGAGT GGCTTGCTTT GCCTGTGGTG GAAAATTGAG CAATTGGGAA CCGAAGGATA      780

ATGCTATGTC AGAACACCTG AGACATTTTC CCAAATGCCC ATTTATAGAA AATCAGCTTC      840

AAGACACTTC AAGATACACA GTTTCTAATC TGAGCATGCA GACACATGCA GCCCGCTTTA      900

AAACATTCTT TAACTGGCCC TCTAGTGTTC TAGTTAATCC TGAGCAGCTT GCAAGTGCGG      960

GTTTTTATTA TGTGGGTAAC AGTGATGATG TCAAATGCTT TTGCTGTGAT GGTGGACTCA     1020

GGTGTTGGGA ATCTGGAGAT GATCCATGGG TTCAACATGC CAAGTGGTTT CCAAGGTGTG     1080

AGTACTTGAT AAGAATTAAA GGACAGGAGT TCATCCGTCA AGTTCAAGCC AGTTACCTC      1140

ATCTACTTGA ACAGCTGCTA TCCACATCAG ACAGCCCAGG AGATGAAAAT GCAGAGTCAT     1200

CAATTATCCA TTTTGAACCT GGAGAACACC ATTCAGAAGA TGCAATCATG ATGAATACTC     1260

CTGTGATTAA TGCTGCCGTG GAAATGGGCT TTAGTAGAAG CCTGGTAAAA CAGACAGTTC     1320

AGAGAAAAAT CCTAGCAACT GGAGAGAATT ATAGACTAGT CAATGATCTT GTGTTAGACT     1380

TACTCAATGC AGAAGATGAA ATAAGGGAAG AGGAGAGAGA AAGAGCAACT GAGGAAAAAG     1440

AATCAAATGA TTTATTATTA ATCCGGAAGA ATAGAATGGC ACTTTTTCAA CATTTGACTT     1500

GTGTAATTCC AATCCTGGAT AGTCTACTAA CTGCCGGAAT TATTAATGAA CAAGAACATG     1560

ATGTTATTAA ACAGAAGACA CAGACGTCTT TACAAGCAAG AGAACTGATT GATACGATTT     1620

TAGTAAAAGG AAATATTGCA GCCACTGTAT TCAGAAACTC TCTGCAAGAA GCTGAAGCTG     1680

TGTTATATGA GCATTTATTT GTGCAACAGG ACATAAAATA TATTCCCACA ·GAAGATGTTT     1740

CAGATCTACC AGTGGAAGAA CAATTGCGGA GACTACAAGA AGAAAGAACA TGTAAAGTGT     1800
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```
GTATGGACAA AGAAGTGTCC ATAGTGTTTA TTCCTTGTGG TCATCTAGTA GTATGCAAAG    1860

ATTGTGCTCC TTCTTTAAGA AAGTGTCCTA TTTGTAGGAG TACAATCAAG GGTACAGTTC    1920

GTACATTTCT TTCATGAAGA AGAACCAAAA CATCATCTAA ACTTTAGAAT TAATTTATTA    1980

AATGTATTAT AACTTTAACT TTCATCCTAA TTTGGTTTCC TTAAAATTTT TATTTATTTA    2040

CAACTCAACA AACATTGTTT TGTGTAACAT ATTTAATATA TGTATCTAAA CCATATGAAC    2100

ATATATTTTT TAGAAACTAA GAGAATGATA GGCTTTTGTT CTTATGAACG AAAAAGAGGT    2160

AGCACTACAA ACACAATATT CAATCAAAAT TTCAGCATTA TTGAAATTGT AAGTGAAGTA    2220

AAACTTAAGA TATTTGAGTT AACCTTTAAG AATTTTAAAT ATTTTGGCAT TGTACTAATA    2280

CCGGGAACAT GAAGCCAGGT GTGGTGGTAT GTGCCTGTAG TCCCAGGCTG AGGCAAGAGA    2340

ATTACTTGAG CCCAGGAGTT TGAATCCATC CTGGGCAGCA TACTGAGACC CTGCCTTTAA    2400

AAACAAACAG AACAAAAACA AAACACCAGG GACACATTTC TCTGTCTTTT TTGATCAGTG    2460

TCCTATACAT CGAAGGTGTG CATATATGTT GAATGACATT TTAGGGACAT GGTGTTTTTA    2520

TAAAGAATTC TGTGAGAAAA AATTTAATAA AACCCCCCAA ATTAAAAAAA AAAAAAAAAA    2580

AAAAAAAAAA AAAAAAAAAA A                                             2601
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 604 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

    Met Asn Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met Lys Ser
    1   5   10   15

    Ala Asn Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu Tyr Arg
                    20   25   30

    Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg
                35   40   45

    Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val
        50   55   60

    Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp
    65   70   75   80
```

Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser Cys Arg Phe Val
                    85                  90                      95

Gln Ser Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln Pro Thr
                100                 105                 110

Phe Pro Ser Ser Val Thr Asn Ser Thr His Ser Leu Leu Pro Gly Thr
            115                 120                 125

Glu Asn Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro Ser Asn
    130                 135                 140

Pro Val Asn Ser Arg Ala Asn Gln Asp Phe Ser Ala Leu Met Arg Ser
145                 150                 155                 160

Ser Tyr His Cys Ala Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe
                165                 170                 175

Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Lys Ala
            180                 185                 190

Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys
        195                 200                 205

Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu
    210                 215                 220

His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln
225                 230                 235                 240

Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala
                245                 250                 255

Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn
                260                 265                 270

Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
        275                 280                 285

Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
        290                 295                 300

Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
305                 310                 315                 320

Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
                325                 330                 335

Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
            340                 345                 350

Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Phe Glu Pro Gly Glu
    355                 360                 365

Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile Asn Ala
    370                 375                 380

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```
Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr Val Gln
385           390           395                   400

Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn Asp Leu
            405           410                   415

Val Leu Asp Leu Leu Asn Ala Glu Asp Glu Ile Arg Glu Glu Glu Arg
        420           425               430

Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Leu Ile Arg
        435           440           445

Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile Pro Ile
450           455               460

Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp
465           470           475               480

Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile
        485           490               495

Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn
        500           505           510

Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln
    515           520           525

Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val
    530           535           540

Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys
545           550           555               560

Met Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val
            565           570               575

Val Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg
        580           585               590

Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
    595           600
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 55 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Cys Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val
1           5               10              15
```

```
Pro Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly
        20          25                      30

Val Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn
        35              40                  45

Trp Lys Leu Gly Asp Ser Pro
    50              55
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 55 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Cys Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val
1               5               10              15

Pro Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly
        20          25                      30

Val Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn
        35              40                  45

Trp Lys Arg Gly Asp Ser Pro
    50              55
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala
1               5               10              15

Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asp
        20              25                  30

Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys Pro Phe
        35              40                  45
```

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Ala Lys Ala Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala
1   5   10   15

Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn
        20   25   30

Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys Pro Phe
        35   40   45

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg Asn Asp
1   5   10   15

Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
        20   25   30

Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg Cys Glu
        35   40   45

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 48 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
1               5               10              15

Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
            20              25              30

Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
        35              40              45
```


(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Glu Glu Arg Thr Cys Lys Val Cys Met Asp Lys Glu Val Ser Val Val
1               5               10              15

Phe Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser
            20              25              30

Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile Ile Lys Gly Thr Val Arg
        35              40              45

Thr Phe Leu Ser
    50
```


(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 52 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Glu Glu Arg Thr Cys Lys Val Cys Met Asp Lys Glu Val Ser Ile Val
1               5               10              15

Phe Ile Pro Cys Gly His Leu Val Val Cys Lys Asp Cys Ala Pro Ser
            20              25              30
```

```
Leu Arg Lys Cys Pro Ile Cys Arg Ser Thr Ile Lys Gly Thr Val Arg
    35              40              45

Thr Phe Leu Ser
    50
```

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2862 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
TTCCTTTACA GTGAATACTG TAGTCTTAAT AGACCTGAGC TGACTGCTGC AGTTGATGTA     60

AGCCACTTTA GAGAATACTG TATGACATCT TCTCTAAGGA AAACCAGCTG CAGACTTCAC    120

TCAGTTCCTT TCATTTCATA GGAAAAGGAG TAGTTCAGAT GTCATGTTTA AGTCCTTATA    180

AGGGAAAAGA GCCTGAATAT ATGCCCTAGT ACCTAGGCTT CATAACTAGT AATAAGAAGT    240

TAGTTATGGG TAAATAGATC TCAGGTTACC CAGAAGAGTT CATGTGACCC CCAAAGAGTC    300

CTAACTAGTG TCTTGGCAAG TGAGACAGAT TTGTCCTGTG AGGGTGTCAA TTCACCAGTC    360

CAAGCAGAAG ACAATGAATC TATCCAGTCA GGTGTCTGTG GTGGAGATCT AGTGTCAAGT    420

GGTGAGAAAC TTCATCTGGA AGTTTAAGCG GTCAGAAATA CTATTACTAC TCATGGACAA    480

AACTGTCTCC CAGAGACTCG GCCAAGGTAC CTTACACCAA AAACTTAAAC GTATAATGGA    540

GAAGAGCACA ATCTTGTCAA ATTGGACAAA GGAGAGCGAA GAAAAAATGA AGTTTGACTT    600

TTCGTGTGAA CTCTACCGAA TGTCTACATA TTCAGCTTTT CCCAGGGGAG TTCCTGTCTC    660

AGAGAGGAGT CTGGCTCGTG CTGGCTTTTA TTATACAGGT GTGAATGACA AAGTCAAGTG    720

CTTCTGCTGT GGCCTGATGT TGGATAACTG GAAACAAGGG GACAGTCCTG TTGAAAAGCA    780

CAGACAGTTC TATCCCAGCT GCAGCTTTGT ACAGACTCTG CTTTCAGCCA GTCTGCAGTC    840

TCCATCTAAG AATATGTCTC CTGTGAAAAG TAGATTTGCA CATTCGTCAC CTCTGGAACG    900

AGGTGGCATT CACTCCAACC TGTGCTCTAG CCCTCTTAAT TCTAGAGCAG TGGAAGACTT    960

CTCATCAAGG ATGGATCCCT GCAGCTATGC CATGAGTACA GAAGAGGCCA GATTTCTTAC   1020

TTACAGTATG TGGCCTTTAA GTTTTCTGTC ACCAGCAGAG CTGGCCAGAG CTGGCTTCTA   1080

TTACATAGGG CCTGGAGACA GGGTGGCCTG TTTTGCCTGT GGTGGGAAAC TGAGCAACTG   1140
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GGAACCAAAG GATGATGCTA TGTCAGAGCA CCGCAGACAT TTTCCCCACT GTCCATTTCT      1200

GGAAAATACT TCAGAAACAC AGAGGTTTAG TATATCAAAT CTAAGTATGC AGACACACTC      1260

TGCTCGATTG AGGACATTTC TGTACTGGCC ACCTAGTGTT CCTGTTCAGC CCGAGCAGCT      1320

TGCAAGTGCT GGATTCTATT ACGTGGATCG CAATGATGAT GTCAAGTGCT TTTGTTGTGA      1380

TGGTGGCTTG AGATGTTGGG AACCTGGAGA TGACCCCTGG ATAGAACACG CCAAATGGTT      1440

TCCAAGGTGT GAGTTCTTGA TACGGATGAA GGGTCAGGAG TTTGTTGATG AGATTCAAGC      1500

TAGATATCCT CATCTTCTTG AGCAGCTGTT GTCCACTTCA GACACCCCAG GAGAAGAAAA      1560

TGCTGACCCT ACAGAGACAG TGGTGCATTT TGGCCCTGGA GAAAGTTCGG AAGATGTCGT      1620

CATGATGAGC ACGCCTGTGG TTAAAGCAGC CTTGGAAATG GGCTTCAGTA GGAGCCTGGT      1680

GAGACAGACG GTTCAGCGGC AGATCCTGGC CACTGGTGAG AACTACAGGA CCGTCAATGA      1740

TATTGTCTCA GTACTTTTGA ATGCTGAAGA TGAGAGAAGA GAAGAGGAGA AGGAAAGACA      1800

GACTGAAGAG ATGGCATCAG GTGACTTATC ACTGATTCGG AAGAATAGAA TGGCCCTCTT      1860

TCAACAGTTG ACACATGTCC TTCCTATCCT GGATAATCTT CTTGAGGCCA GTGTAATTAC      1920

AAAACAGGAA CATGATATTA TTAGACAGAA AACACAGATA CCCTTACAAG CAAGAGAGCT      1980

TATTGACACC GTTTTAGTCA AGGGAAATGC TGCAGCCAAC ATCTTCAAAA ACTCTCTGAA      2040

GGAAATTGAC TCCACGTTAT ATGAAAACTT ATTTGTGGAA AAGAATATGA AGTATATTCC      2100

AACAGAAGAC GTTTCAGGCT TGTCATTGGA AGAGCAGTTG CGGAGATTAC AAGAAGAACG      2160

AACTTGCAAA GTGTGTATGG ACAGAGAGGT TTCTATTGTG TTCATTCCGT GTGGTCATCT      2220

AGTAGTCTGC CAGGAATGTG CCCCTTCTCT AAGGAAGTGC CCCATCTGCA GGGGGACAAT      2280

CAAGGGGACT GTGCGCACAT TTCTCTCATG AGTGAAGAAT GGTCTGAAAG TATTGTTGGA      2340

CATCAGAAGC TGTCAGAACA AAGAATGAAC TACTGATTTC AGCTCTTCAG CAGGACATTC      2400

TACTCTCTTT CAAGATTAGT AATCTTGCTT TATGAAGGGT AGCATTGTAT ATTTAAGCTT      2460

AGTCTGTTGC AAGGGAAGGT CTATGCTGTT GAGCTACAGG ACTGTGTCTG TTCCAGAGCA      2520

GGAGTTGGGA TGCTTGCTGT ATGTCCTTCA GGACTTCTTG GATTTGGAAT TTGTGAAAGC      2580

TTTGGATTCA GGTGATGTGG AGCTCAGAAA TCCTGAAACC AGTGGCTCTG GTACTCAGTA      2640

GTTAGGGTAC CCTGTGCTTC TTGGTGCTTT TCCTTTCTGG AAAATAAGGA TTTTTCTGCT      2700

ACTGGTAAAT ATTTTCTGTT TGTGAGAAAT ATATTAAAGT GTTTCTTTTA AAGGCGTGCA      2760

TCATTGTAGT GTGTGCAGGG ATGTATGCAG GCAAACACT GTGTATATAA TAAATAAATC       2820

TTTTTAAAAA GTGAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                        2862
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(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 612 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Met Asp Lys Thr Val Ser Gln Arg Leu Gly Gln Gly Thr Leu His Gln
1               5                   10                  15

Lys Leu Lys Arg Ile Met Glu Lys Ser Thr Ile Leu Ser Asn Trp Thr
            20              25                  30

Lys Glu Ser Glu Glu Lys Met Lys Phe Asp Phe Ser Cys Glu Leu Tyr
            35              40                  45

Arg Met Ser Thr Tyr Ser Ala Phe Pro Arg Gly Val Pro Val Ser Glu
    50              55                  60

Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
65              70              75                  80

Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Gln Gly
            85              90                  95

Asp Ser Pro Val Glu Lys His Arg Gln Phe Tyr Pro Ser Cys Ser Phe
        100             105             110

Val Gln Thr Leu Leu Ser Ala Ser Leu Gln Ser Pro Ser Lys Asn Met
        115             120             125

Ser Pro Val Lys Ser Arg Phe Ala His Ser Ser Pro Leu Glu Arg Gly
    130             135             140

Gly Ile His Ser Asn Leu Cys Ser Ser Pro Leu Asn Ser Arg Ala Val
145             150             155             160

Glu Asp Phe Ser Ser Arg Met Asp Pro Cys Ser Tyr Ala Met Ser Thr
            165             170             175

Glu Glu Ala Arg Phe Leu Thr Tyr Ser Met Trp Pro Leu Ser Phe Leu
        180             185             190

Ser Pro Ala Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
    195             200             205

Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
210             215             220

Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro His Cys
225             230             235             240
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Pro Phe Leu Glu Asn Thr Ser Glu Thr Gln Arg Phe Ser Ile Ser Asn
                245                 250             255

Leu Ser Met Gln Thr His Ser Ala Arg Leu Arg Thr Phe Leu Tyr Trp
            260             265             270

Pro Pro Ser Val Pro Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe
            275             280             285

Tyr Tyr Val Asp Arg Asn Asp Asp Val Lys Cys Phe Cys Cys Asp Gly
    290             295             300

Gly Leu Arg Cys Trp Glu Pro Gly Asp Asp Pro Trp Ile Glu His Ala
305             310             315                 320

Lys Trp Phe Pro Arg Cys Glu Phe Leu Ile Arg Met Lys Gly Gln Glu
            325             330             335

Phe Val Asp Glu Ile Gln Ala Arg Tyr Pro His Leu Leu Glu Gln Leu
            340             345             350

Leu Ser Thr Ser Asp Thr Pro Gly Glu Glu Asn Ala Asp Pro Thr Glu
    355             360             365

Thr Val Val His Phe Gly Pro Gly Glu Ser Ser Glu Asp Val Val Met
    370             375             380

Met Ser Thr Pro Val Val Lys Ala Ala Leu Glu Met Gly Phe Ser Arg
385             390             395                 400

Ser Leu Val Arg Gln Thr Val Gln Arg Gln Ile Leu Ala Thr Gly Glu
            405             410             415

Asn Tyr Arg Thr Val Asn Asp Ile Val Ser Val Leu Leu Asn Ala Glu
            420             425             430

Asp Glu Arg Arg Glu Glu Glu Lys Glu Arg Gln Thr Glu Glu Met Ala
    435             440             445

Ser Gly Asp Leu Ser Leu Ile Arg Lys Asn Arg Met Ala Leu Phe Gln
    450             455             460

Gln Leu Thr His Val Leu Pro Ile Leu Asp Asn Leu Leu Glu Ala Ser
465             470             475                 480

Val Ile Thr Lys Gln Glu His Asp Ile Ile Arg Gln Lys Thr Gln Ile
            485             490             495

Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr Val Leu Val Lys Gly Asn
            500             505             510

Ala Ala Ala Asn Ile Phe Lys Asn Ser Leu Lys Glu Ile Asp Ser Thr
            515             520             525

Leu Tyr Glu Asn Leu Phe Val Glu Lys Asn Met Lys Tyr Ile Pro Thr
    530             535             540
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Glu Asp Val Ser Gly Leu Ser Leu Glu Glu Gln Leu Arg Arg Leu Gln
545             550                 555                     560

Glu Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val
            565                 570                 575

Phe Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser
            580                 585                 590

Leu Arg Lys Cys Pro Ile Cys Arg Gly Thr Ile Lys Gly Thr Val Arg
        595                 600                 605

Thr Phe Leu Ser
    610
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